

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: November 4, 2002, 01:54:20 ; Search time 47.6067 Seconds  
(without alignments)  
1592.744 Million cell updates/sec

Title: US-09-805-550-4

Perfect score: 1910  
Sequence: 1 MKLVKTKLKGTHFEIRVOPN.....CDNEELANYLEHAERD 368

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

SPREMBL\_21.\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rotent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query	Match length	DB	ID	Description
1	1169.5	61.2	365	10	094CE9	094CE9 arabidopsis
2	1153.5	60.4	379	10	003991	003991 daucus caro
3	1043.5	54.6	367	10	09MA10	09MA10 arabidopsis
4	1019	53.4	389	10	09STA6	09STA6 lycopersico
5	978	51.2	419	10	09M887	09M887 arabidopsis
6	954	49.9	382	10	003990	003990 daucus caro
7	931.5	48.8	378	10	09FE16	09FE16 arabidopsis
8	930.5	48.7	378	10	094C35	094C35 arabidopsis
9	887.5	46.5	392	10	040742	040742 oryza sativ
10	861.5	34.6	246	10	09S9L8	09S9L8 arabidopsis
11	621.5	32.5	409	4	08W0B0	08W0B0 homo sapien
12	490.5	25.7	414	5	09XZ0	09XZ0 drosophila
13	487.5	25.5	414	5	09V3W9	09V3W9 drosophila
14	484	25.3	341	5	097135	097135 dictyostel
15	424	22.2	113	10	09SA20	09SA20 arabidopsis
16	405	21.2	372	5	023451	023451 caenorhabd

17	405	21.2	748	6	P79370	P79370 oryctolagus
18	375	19.6	230	5	09VCD5	09VCD5 drosophila
19	323	11.3	523	5	09NIF3	09NIF3 dictyostel
20	214	11.2	575	10	09EFM5	09EFM5 oryza sativ
21	204.5	10.7	142	10	09LE19	09LE19 arabidopsis
22	201	10.5	551	10	09S1I8	09S1I8 arabidopsis
23	201	10.5	551	10	094C51	094C51 arabidopsis
24	194.5	10.2	538	10	09S1I9	09S1I9 arabidopsis
25	193	10.1	65	10	09SCA8	09SCA8 lycopersico
26	180.5	9.5	582	11	09QZM1	09QZM1 mus musculus
27	176	9.2	589	4	09H0T8	09H0T8 homo sapien
28	176	9.2	589	4	09UMX0	09UMX0 homo sapien
29	174	9.1	595	6	09S5M9	09S5M9 bos taurus
30	171	9.0	601	4	09NRR5	09NRR5 homo sapien
31	170.5	8.9	602	11	09JUP9	09JUP9 rattus norv
32	170.5	8.9	596	11	099NB8	099NB8 mus musculus
33	169	8.8	314	4	09H8R7	09H8R7 homo sapien
34	167.5	8.8	582	11	08R317	08R317 mus musculus
35	167	8.7	638	11	09Q2M0	09Q2M0 mus musculus
36	165	8.6	589	4	09H3R4	09H3R4 caenorhabd
37	163.5	8.6	502	5	018672	018672 caenorhabd
38	155.5	8.1	101	5	09GZJ7	09GZJ7 trypanosoma
39	155	8.1	915	5	026872	026872 trypanosoma
40	150	7.9	585	13	09PVN8	09PVN8 xenopus lae
41	150	7.9	624	4	09UH09	09UH09 homo sapien
42	150	7.9	624	4	09HAZ4	09HAZ4 homo sapien
43	147.5	7.7	902	10	09FH07	09FH07 arabidopsis
44	140	7.3	701	13	091890	091890 xenopus lae
45	137.5	7.2	349	12	09DT22	09DT22 chlorella v

## ALIGNMENTS

RESULT 1  
ID Q94CE9 PRELIMINARY; PRT; 365 AA.  
AC Q94CE9;  
DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
DE Putative RAD23 protein.  
GN F20B17.8.  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliopsida; eudicotyledons; core eudicots; rosidae;  
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
OX NCBI\_TaxID=3702;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,  
RA Goldsmith A.D., Lee J.M., Quach H.L., Tang C., Toriumi M., Yu G.,  
RA Bowser L., Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J.,  
RA Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Koeseima E.,  
RA Lam B., Lin J., Meyers M.C., Miranda M., Narusaka M., Nguyen M.,  
RA Palm C.J., Sakurai T., Satou M., Seki M., Shinn P., Southwick A.,  
RA Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;  
RT Submitted length cDNA of gene F20B17.8 (GI:7715605).";  
RT Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Yamada K., Banh J., Banno F., Chang E., Dale J.M., Goldsmith A.D.,  
RA Lee J.M., Onodera C.S., Quach H.L., Tang C., Toriumi M., Wu H.C.,  
RA Yamanura Y., Yu G., Yu S., Bowser L., Carninci P., Chen H., Cheuk R.,  
RA Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,  
RA Kawai J., Kim C., Koeseima E., Lam B., Lin J., Meyers M.C., Miranda M.,  
RA Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M.,  
RA Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,  
RT Theologis A.;  
RT "Full length cDNA of gene F20B17.8 (GI:7715605).";  
RT Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY034912; AAK59419.1; -;  
DR EMBL; AY063103; AAL34277.1; -;

Query Match	61.2%	Score 1169.5	DB 10	Length 365
Best Local Similarity	65.1%	Pred. No. 2.6e-72		
Matches 246	Conservative 43	Mismatches 66	Indels 23	Gaps 9
DR InterPro: IPR004806; Rad23.				
DR InterPro: IPR000449; UBA_domain.				
DR InterPro: IPR000626; Ubiqultin.				
DR Pfam: PF00627; UBA; 2.				
DR Pfam: PF00240; ubiquitin; 1.				
DR TIGRFAMs: TIGR00601; rad23; 1.				
DR PROSITE: PS0053; UBIQUITIN_2; 1.				
DR SEQUENCE 365 AA; 39157 MW; 4FED9EC59B467745 CRC64;				
Query Match	61.2%	Score 1169.5	DB 10	Length 365
Best Local Similarity	65.1%	Pred. No. 2.6e-72		
Matches 246	Conservative 43	Mismatches 66	Indels 23	Gaps 9
DR InterPro: IPR004806; Rad23.				
DR InterPro: IPR000449; UBA_domain.				
DR InterPro: IPR000626; Ubiqultin.				
DR Pfam: PF00627; UBA; 2.				
DR Pfam: PF00240; ubiquitin; 1.				
DR TIGRFAMs: TIGR00601; rad23; 1.				
DR PROSITE: PS0053; UBIQUITIN_2; 1.				
DR SEQUENCE 365 AA; 39157 MW; 4FED9EC59B467745 CRC64;				

DR PROSITE: PS50053; UNIOJITN.2: 1  
SQ SEQUENCE 379 AA; 40530 MW; B26697BA39CC5929 CMC64;  
Query Match 60.4%; Score 1153.5; DB 10; Length 379;  
Best Local Similarity 63.0%; Pred. No. 3.5e-71;  
Matches 240; Conservative 45; Mismatches 81; Indels 15; Gaps 9;

QY 1 MKLVTKTKGTHFEELRVQPNPDIMAVKKNIEIOCKDSYPMGQOLLINQVLYKDESTLE 60  
DB 1 MKLVTKTKGSHFEELRVQPNPDIMAVKKNIEIOCKDSYPMGQOLLINQVLYKDESTLE 60  
QY 61 EKKVNEDEGLVYMLSKGTSGTSSSOHSNTPTPAQAP---PLEAPQAQPPVPAPIT 117  
DB 61 ESKIEDDEGLVYMLGSKSTMSTGTPAAQSSAPAPTPAPAVAPAPAPAAASAVIYNT 120  
QY 118 TSQAQAP-LPAQAP-NTHDMAANLISGRNVDITIIQLEMGGSMGXDKYQALRAAYN 174  
DB 121 TV-VPAPLSPAPAFAPSDTYGEAASNVVAGSNLEQTIQHIMDGGMWDITNNVSRALRAAYN 179  
QY 175 NPERAVELTSGIPYTAETIANPVG---GOGANTTDRA--PTGEGAGLS-GIPTAPLDFP 228  
DB 180 NPERAVADLYTSGIPPMARAAAPVSHFDQDIINAGNNAISDGVACAPGAPSNISLPMFP 239  
QY 229 QGASNAGGAGGAGGPPDLFTRNPNQFQAVREMYHTNPQIILQPMIYELSKONPQILRIEENH 288  
DB 240 QETLSGTGTAGAGSLEFLRNPNQFQAVREMYHTNPQIILQPMIYELSKONPQILRIEENH 299  
QY 289 DEFLQLEPEPEGCGEDPLDQPEDEEMHAISVTPPEQBAICRLSEMGFDRARVETAPLA 348  
DB 300 EEFLLQLEPEVYASGDWFDQPEQD-VQPEITVTAAQDEALIERLEAMGFDGLVETAPLA 358  
QY 349 CDRNEELANTILLENHAGE-ED 368  
DB 359 CDRNEELAVNLYLENAGDFED 379

RESULT 3  
Q9MA10 PRELIMINARY; PRT; 367 AA.  
ID Q9MA10  
AC Q9MA10;  
DT 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
DE F20B17.8.  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eucosids II; Brassicales; Brassicaceae; Arabidopsids.  
CX NCBI\_TaxID=3702;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Khan S., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Kim C.,  
RA Shinn P., Altafi H., Bei Q., Chin C., Chlou J., Choi E., Conn L.,  
RA Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B., Lee J.,  
RA Lenz C., Li J., Liu J., Liu K., Liu S., Mukharsky N., Nguyen M.,  
RA Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thayer A.,  
RA Toriunji M., Vayberg M., Yu G., Federspiel N.A., Theologis A.,  
RA Ecker J.R.;  
RT "Genomic sequence for Arabidopsis thaliana BAC F20B17 from chromosome  
RT I.";  
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Ecker J.R.;  
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RA Ecker J.R.;  
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE FROM N.A.  
RA Chauk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,  
RA Khan S., Kim C., Altafi H., Bei B., Chin C., Chlou J., Choi E.,

RA Conn L., Conway A., Gonzalez A., Hansen N., Howling B., Koo T., Lam B.,  
RA Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharly N.,  
RA Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,  
RA Thayer A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N.,  
RA Theologis A., Becker J.;  
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AC010793; AF68123.1; -.  
DR HSSP: P54725; IDV0.  
DR InterPro: IPR004806; Rad23.  
DR InterPro: IPR000449; UBA.domain.  
DR InterPro: IPR000626; Ubiquitin.  
DR Pfam: PF00627; UBA; 2.  
DR Pfam: PF00240; ubiquitin; 1.  
DR SMART: SM00165; UBA; 2.  
DR SMART: SM00213; UBO; 1.  
DR TIGRFAMs: TIGR00601; rad23; 1.  
DR PROSITE: PSS0053; UBIOUITIN\_2; 1.  
SQ SEQUENCE 367 AA; 39790 MW; C6D01134B5C69CE6 CRC64;

Query Match 54.6%; Score 1043.5; DB 10; Length 367;  
Best Local Similarity 59.3%; Pred. No. 1.1e-63;  
Matches 232; Conservative 39; Mismatches 73; Indels 47; Caps 11;

QY 1 MKLVKTLKGTHFEIRVPNDITMAVKKNIEIGKDSYPMGQOLLFNGKVLDESTLE 60  
DB 1 MKLVKTLKSHFEIRVLPDITMAVKKNIEDSGKDNYPGQQLLHNGVLDDETSLV 60  
QY 61 ENKYNEDGFLVYMLSKGTSSTGSSQ-----HSNTPATROAPLEAPQAPPPV 113  
DB 61 ENKTEGEGFLVYMLSKSGSGSAGQASVQCYRLLFHSLFP-----LPHRLSLSY 111  
QY 114 APIT-----SQPEGLPAQAPNTHDNANSLSGRNVDITINQLEMGGSGMDKDV 165  
DB 112 NPVPTSCFTYSCRTTG-----TDYTGQAASLTVSGSLQVQQLMEMGGSGMDKTV 166  
QY 166 QRARAAVNNPERAVELYSGIPYTAETP-----IGGCGANTTDAPTEAGLSGTPN 220  
DB 167 TRARAAVNNPERAVDLYSGIPQTAAYVAVPEAQAIGSQA-----APVAPA--SGGPN 219  
QY 221 TAPLDLPFGASNAGGAGGGLDFLRNNPQFOAVREKVNHTNPQILDPMLVELSKONPQI 280  
DB 220 SSPDLDFPQEVAAAGSGDGLTEFLRNNQVAIL--TISFSLNCEPMLOELGKQNPQL 277  
QY 281 LRLIEHNDEFLOLNEPFEG--GEGDFLDQPEDEMPHAISVTPPEQEAIGRLSEMGFD 338  
DB 278 LRLIQENQAEFLQLVNPEYEGSDGDMFDQPEQ--EMPHAINVPAQDEAIGRLSEMGFD 336  
QY 339 RARVTEAFACDRNEELANYLEHAGE-ED 368  
DB 337 RALVTEAFACDRNEELANYLEHAGE-ED 367

## RESULT 4

Q9STA6 PRELIMINARY; PRT; 389 AA.  
AC Q9STA6;  
DT 01-MAY-2000 (TREMblrel. 13, Created)  
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)  
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)  
DE RAD23 protein.  
GN RAD23.  
OS Lycopersicon esculentum (Tomato).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.  
OX NCBI\_TaxID=4081;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CV, WEST VIRGINIA 106; TISSUE=FRUIT;  
RA Lemaire-Chamley M., Petit J., Raymond P., Chevalier C.;  
RT "Analysis of gene expression during early tomato fruit development by  
RT mRNA differential display.";  
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL: AJ243875; CAB51544.1; -.  
DR HSSP: P54725; IDV0.  
DR InterPro: IPR004806; Rad23.  
DR InterPro: IPR000449; UBA.domain.  
DR InterPro: IPR000626; Ubiquitin.  
DR Pfam: PF00627; UBA; 2.  
DR Pfam: PF00240; ubiquitin; 1.  
DR SMART: SM00165; UBA; 2.  
DR SMART: SM00213; UBO; 1.  
DR TIGRFAMs: TIGR00601; rad23; 1.  
DR PROSITE: PSS0053; UBIOUITIN\_2; 1.  
SQ SEQUENCE 389 AA; 41508 MW; D2BAEDFOFE70778A CRC64;

Query Match 53.4%; Score 1019; DB 10; Length 389;  
Best Local Similarity 53.8%; Pred. No. 5.9e-62;  
Matches 214; Conservative 47; Mismatches 97; Indels 40; Caps 6;

QY 1 MKLVKTLKGTHFEIRVPNDITMAVKKNIEIGKDSYPMGQOLLFNGKVLDESTLE 60  
DB 1 MKLVKTLKSHFEIRVLPDITMAVKKNIESVQGDVYPAQOQLHNGKVLDTTLE 60  
QY 61 ENKYNEDGFLVYMLSKGTSSTGSS-----SOHSTPATROAPPL 102  
DB 61 ENKVAENSTFVIMLSKNKVS-STGTSSIALNSTAPDQGSTDAQRTITTPQATLALPQ 119  
QY 103 EAPQAPPPVAPPTTSQPEGLPAQAPNTHDNANSLSGRNVDITINQLEMGGSGMDK 162  
DB 120 SASSEAPTPAPVAPPAAS-----SYVDVYQQAASNLVAGSLNETYQQLIDMGGSGMDR 172  
QY 163 DKVQALRAVNNPERAVELYSGIPYTAETP-----AVPGGCGANTTDAPPT 210  
DB 173 DTVVRAALAAVNNPERAVDLYSGIPEQTEIPVAPARAAPAVTAPASQAINPAQDAS 232  
QY 211 GEAGLSGIPNTAPLDLPFGASNAGGAGGGLDFLRNNPQFOAVREKVNHTNPQILPML 270  
DB 233 QLAVPSSGPNAPLDLPFGGLTNGSNAGNLDPLRNSPQFOALRAVQANPQILPML 292  
QY 271 VELSKONPQILRLIEHNDEFLOLNEPFEGEGDFLDQPEDEMPHAISVTPPEQEAIG 330  
DB 293 QELGQNQNHMLRLQEHQPDFLRLINEPVE--GEGVNLQO--TAGALPQAVTTPPEREAIE 350  
QY 331 RLESKGFPRARVTEAFACDRNEELANYLEHAGEED 368  
DB 351 RLEAMGFDRALVLEYEFACNKRNEELANYLEHHEFD 388

## RESULT 5

Q9M887 PRELIMINARY; PRT; 419 AA.  
AC Q9M887;  
DT 01-OCT-2000 (TREMblrel. 15, Created)  
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)  
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)  
DE Putative RAD23 (At3g02540/F16B3\_17).  
GN F16B3\_17.  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
OX NCBI\_TaxID=3702;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CV, COLUMBIA;  
RA Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B., Wu D.,  
RA Rongling C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E.,  
RA Bowman C.B., White O., Nierman W.C., Fraser C.M.;  
RT "Arabidopsis thaliana chromosome III BAC F16B3 genomic sequence.";  
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC Kim C.J., Chen H., Cheuk R., Koesema E., Meyers M.C., Banh J.,  
RA Bowser L., Carninci P., Dale J.M., Gibson H.A., Goldsmith A.D.,  
RA Hayashizaki Y., Ishida J., Jiang P.X., Jones T., Kamiya A.,

RA Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X.,  
RA Miranda M., Narusaka M., Nguyen M., Onodera C.S., Palm C.J.,  
RA Pham P.K., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,  
RA Tang C.C., Toriumi M., Yamada K., Yu G., Yu S., Shinozaki K.,  
RA Davis R.W., Theologis A., Ecker J.R.,  
RT "Arabidopsis cDNA clones,"  
RT Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AC021640; AF32461.1;  
DR EMBL: AY039562; AK62617.1;  
DR HSSP: P54725; IDV0.  
DR InterPro: IPR002965; P-rich\_extensu.  
DR InterPro: IPR004806; Rad23.  
DR InterPro: IPR000449; UBA\_domain.  
DR InterPro: IPR000626; Ubiquitin.  
DR Pfam: PF00627; UBA; 2.  
DR Pfam: PF00240; ubiquitin; 1.  
DR PRINTS: PRO1217; PRICHEXTENS.  
DR SMART: SM00165; UBA; 2.  
DR SMART: SM00213; UBO; 1.  
DR TIGRFAMs: TIGR00601; rad23; 1.  
DR PROSITE: PS50053; UBIQUITIN\_2; 1.  
SQ SEQUENCE 419 AA; 44247 MW; CAA13BC4FEB1E25 CRC64;

Query Match 51.2%; Score 978; DB 10; Length 419;  
Best Local Similarity 50.6%; Pred No. 4.2e-59;  
Matches 213; Conservative 58; Mismatches 90; Indels 60; Gaps 12;

QY 1 MKLTVTLKGTHEIRVQNDITMAVKNIEIOGKDSYPMGQOLLIFNGKVLKDESTLE 60  
DB 1 MKLTVTLKGTHEIRVQNDITMAVKNIEIOGKDSYPMGQOLLIFNGKVLKDESTLE 60  
QY 61 ENKVNEDGLVYMLSKGKSGTSSSOHSNTPATROAP-----QPPVA- 114  
DB 61 ENKVNEDGLVYMLSKGKSGTSSSOHSNTPATROAP-----QPPVA- 114  
QY 101 -PLEAPQAPPPVAP-----ITTSQPEGLPA-----QAP-----NTHDNAASN 138  
DB 101 -PLEAPQAPPPVAP-----ITTSQPEGLPA-----QAP-----NTHDNAASN 138  
QY 121 APTRPPTAPPTAPPAVATETVTPPIPEVPATISSSTPAPDSAPVSGDVGGAASN 180  
DB 121 APTRPPTAPPTAPPAVATETVTPPIPEVPATISSSTPAPDSAPVSGDVGGAASN 180  
QY 139 LLSGRNVDTTINOLMEMGGSDKDKVQALRAAYNNPERAVEYLSGIPVTAETIAVPI- 197  
DB 139 LLSGRNVDTTINOLMEMGGSDKDKVQALRAAYNNPERAVEYLSGIPVTAETIAVPI- 197  
QY 181 LLAGSMLESTIOOILDMGGTMDRETIVLALRAFNPPRAVEYLYTGIPEQAEVP- 239  
DB 181 LLAGSMLESTIOOILDMGGTMDRETIVLALRAFNPPRAVEYLYTGIPEQAEVP- 239  
QY 198 -----GGGAGNTTDRAPTEAGLSGIPNTAPLDFPQASNMGGGAGGPRDPLFRNNPP 252  
DB 198 -----GGGAGNTTDRAPTEAGLSGIPNTAPLDFPQASNMGGGAGGPRDPLFRNNPP 252  
QY 240 RPPASGQAPNPPAQTOOPAAAPASCPNANPLDFEPQGLPNVNGAGACTDPLFRNSQOF 299  
DB 240 RPPASGQAPNPPAQTOOPAAAPASCPNANPLDFEPQGLPNVNGAGACTDPLFRNSQOF 299  
QY 253 QAVREKVTNPOILOPMLVELSKONFOILRIEENHDEFQILNEPFEKG--EGDFLQD- 309  
DB 253 QAVREKVTNPOILOPMLVELSKONFOILRIEENHDEFQILNEPFEKG--EGDFLQD- 309  
QY 300 QALRAVQANPQVLOPMLDELGNKNMLRLIODHADFLRLINEVEGGESGNLIGQM 359  
DB 300 QALRAVQANPQVLOPMLDELGNKNMLRLIODHADFLRLINEVEGGESGNLIGQM 359  
QY 310 ----PEEDMPHAISVTPPEOEAIGLESMPGFDRAVIEAFLACDRNEELANYLLEHAG 365  
DB 310 ----PEEDMPHAISVTPPEOEAIGLESMPGFDRAVIEAFLACDRNEELANYLLEHAG 365  
QY 366 AAGMPQ----POAIVTHEREAIERLEAMGFERALVLEVFACNKNNEELANYLLDHMH 415  
DB 366 AAGMPQ----POAIVTHEREAIERLEAMGFERALVLEVFACNKNNEELANYLLDHMH 415  
QY 416 E 416

RESULT 6  
003990 PRELIMINARY; PRT; 382 AA.  
AC 003990;  
DT 01-JUL-1997 (TREMBlrel. 04, Created)  
DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)  
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
DE RAD23, isoform 1.  
OS Daucus carota (Carrot).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
OC Asteridae; eusterids II; Apiales; Apiaceae; Daucus.  
OX NCBI\_TaxID=4039;

RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=M001C;  
RX MEDLINE=9834597; PubMed=9681019;  
RA Stum A., Reinhard S.;  
RT "Two isoforms of plant RAD23 complement a UV-sensitive rad23 mutant in yeast."  
RL Plant J. 13:815-821(1998).  
DR EMBL: Y12013; CAA72741.1;  
DR HSSP: P54725; IDV0.  
DR InterPro: IPR004806; Rad23.  
DR InterPro: IPR000449; UBA\_domain.  
DR InterPro: IPR000626; Ubiquitin.  
DR Pfam: PF00627; UBA; 2.  
DR Pfam: PF00240; ubiquitin; 1.  
DR SMART: SM00165; UBA; 2.  
DR SMART: SM00213; UBO; 1.  
DR TIGRFAMs: TIGR00601; rad23; 1.  
DR PROSITE: PS50053; UBIQUITIN\_2; 1.  
SQ SEQUENCE 382 AA; 40344 MW; 27FF02A2402F3DC2 CRC64;

Query Match 49.9%; Score 954; DB 10; Length 382;  
Best Local Similarity 52.4%; Pred No. 1.6e-57;  
Matches 205; Conservative 52; Mismatches 98; Indels 36; Gaps 9;

QY 1 MKLTVTLKGTHEIRVQNDITMAVKNIEIOGKDSYPMGQOLLIFNGKVLKDESTLE 60  
DB 1 MKLTVTLKGTHEIRVQNDITMAVKNIEIOGKDSYPMGQOLLIFNGKVLKDESTLE 60  
QY 61 ENKVNEDGLVYMLSKGKSGTSSSOHSNTPATROAPPLEAPQAP-----QPPVA- 114  
DB 61 ENKVNEDGLVYMLSKGKSGTSSSOHSNTPATROAPPLEAPQAP-----QPPVA- 114  
QY 115 -PITTSQPEGLPAQAP-----NTHDNAASNLISGRNVDTTINOLMEMGGSDKDK 163  
DB 115 -PITTSQPEGLPAQAP-----NTHDNAASNLISGRNVDTTINOLMEMGGSDKDK 163  
QY 117 LVPAPSPAPATAPIPPAAGSEANYSASLLVAGSNLEGAIOOILDMGGGTMDRD 176  
DB 117 LVPAPSPAPATAPIPPAAGSEANYSASLLVAGSNLEGAIOOILDMGGGTMDRD 176  
QY 164 KYQALRAAYNNPERAVEYLSGIPVTAETIAVPI-----GGGAGNTTDRAPPTG--EAGLS 216  
DB 164 KYQALRAAYNNPERAVEYLSGIPVTAETIAVPI-----GGGAGNTTDRAPPTG--EAGLS 216  
QY 177 TVIRIVRAAFNPPRAVEYLSGIPVTAETIAVPI-----GGGAGNTTDRAPPTG--EAGLS 235  
DB 177 TVIRIVRAAFNPPRAVEYLSGIPVTAETIAVPI-----GGGAGNTTDRAPPTG--EAGLS 235  
QY 217 GIPNTAPLDFPQASNMGG--GGAGGPRDPLFRNNPOFQAVREKVTNPOILOPMLVELSK 275  
DB 217 GIPNTAPLDFPQASNMGG--GGAGGPRDPLFRNNPOFQAVREKVTNPOILOPMLVELSK 275  
QY 236 AGPNANPLDFPQGLPDMKSNAGANLDFLTNOQFALRAVQSNPOIILPMLQELGK 295  
DB 236 AGPNANPLDFPQGLPDMKSNAGANLDFLTNOQFALRAVQSNPOIILPMLQELGK 295  
QY 276 QNPOLRLIEENHDEFQILNEPFEKGEGDFLDQPEEDMPHAISVTPPEOEAIGRLISM 335  
DB 276 QNPOLRLIEENHDEFQILNEPFEKGEGDFLDQPEEDMPHAISVTPPEOEAIGRLISM 335  
QY 296 QNPMLRLIOHQADFQILNEPMEGENTL-----GHGPAISVTPPEOEAIGRLISM 349  
DB 296 QNPMLRLIOHQADFQILNEPMEGENTL-----GHGPAISVTPPEOEAIGRLISM 349  
QY 336 GFDRAVIEAFLACDRNEELANYLLEHAGE 366  
DB 336 GFDRAVIEAFLACDRNEELANYLLEHAGE 366  
QY 350 GFDRELIVLEVFACNKNNEELANYLLDHME 380  
DB 350 GFDRELIVLEVFACNKNNEELANYLLDHME 380

RESULT 7  
09FF16 PRELIMINARY; PRT; 378 AA.  
AC 09FF16;  
DT 01-MAR-2001 (TREMBlrel. 16, Created)  
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
DE DNA repair protein RAD23 homolog (Hypothetical 40.1 kDa protein) (At5g38470/At5g38470).  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC Eucosids II; Brassicales; Brassicaceae; Arabidopsis.  
OX NCBI\_TaxID=3702;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=COLUMBIA;  
RX MEDLINE=97471969; PubMed=9330910;  
RA Sato S., Kotani H., Nakamura T., Kaneko T., Asamizu E., Fukami M.,



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RESULT 9
ID Q40742 PRELIMINARY; PRT; 392 AA.
AC Q40742;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE OSRAD23.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
NCBI_TaxID=4530;
RN
  (1)
  RC SEQUENCE FROM N.A.
  RC STRAIN=NIPPONBARE;
  RX MEDLINE=97369378; PubMed=9225866;
  RA Schultze T.F., Quatrano R.S.;
  RT "Characterization and expression of a rice RAD23 gene.";
  RL Plant Mol. Biol. 34:557-562(1997).
  DR EMBL; 063530; AAB65841.1; -.
  DR HSSP; P54725; IDV0.
  DR InterPro; IPR004806; Rad23.
  DR InterPro; IPR000626; Ubiquitin.
  DR Pfam; PF0627; UBA; 2.
  DR Pfam; PF00240; ubiquitin; 1.
  DR SMART; SM00165; UBA; 2.
  DR SMART; SM00213; UBO; 1.
  DR TIGRPSMs; TIGR00601; rad23; 1.
  DR PROSITE; PS50053; UBIQUITIN_2; 1.
  DR PROSITE; PS50053; UBIQUITIN_2; 1.
  SQ SEQUENCE 392 AA; 41754 MW; BDE08574CC7ACB CRC64;

Query Match
Best Local Similarity 46.5%; Score 887.5; DB 10; Length 392;
Best Local Similarity 50.9%; Pred. No. 66-53;
Matches 199; Conservative 52; Mismatches 109; Indels 31; Gaps 10;

OY 1 MKLTVTKLGTGHEIRVOPNDITMAVKKNIETIOGDSYPMGQOLLIFNGKYLKDESTLE 60
DB 1 MKISVTKLGSTFEIOLVDSAQKAVADYKRIETITOGQHIYPAEQOMLIHQGKVLKDDTTL 60
OY 61 ENKVNEDGFLVYMLSKGTSGTSSQSHSNTPATROAPLEAPQAP--QPPVAPITTT 118
DB 61 ENKVNEDGFLVYMLSKGTSGTSSQSHSNTPATROAPLEAPQAP--QPPVAPITTT 118
OY 119 -----SOEGCLPAQAP-----NTHDNAANLLSGRNVDTITNOLMEMGGSGMDK 163
DB 117 VPTVTSAPPTTATSPAPAVAVSSEADNTGQATSNLVAAGSNLEATITQSTILEMGGIMDKD 176
OY 164 KQORALRAAYNNPERAVELYSGIPYTAETAVPIGG--QGANTTTDRA---PTGEAGLSGI 218
DB 177 IYVHAISAFAFNPERAVELYSGVPEQMDIPVPPSIQNPANPTQASQATQAPAPSTLSSG 236
OY 219 PNTAPLDEPPQASNAGGAGG--GPLDFLRNPPQQAQVEMVHTNQITQPMVLVELSKG 277
DB 237 PNASPLDLPQALPNASTDAAGIGNDALRNNAQFETLLSLVQANQIILQPLQELGKGN 296
OY 278 PQILRLIEENHDEFLQILNEPEEG--GEGDFLDQ--PEDEMPHAI SVTPPEOFAIGLEEM 335
DB 297 PQIQLQIQENQAEFLALINERPAEGDDEENLDOQFE--AMPQTIATVPDEDAIILRLFP 354
OY 336 GEDRAVIEAPLACDRNEELAAVYLLRHAGE 366
DB 355 GEDRALVLDVFFACNKDEQLAANYLLDHMNE 385

RESULT 10
ID Q9S9L8 PRELIMINARY; PRT; 246 AA.
AC Q9S9L8;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)

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DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE T24D18.27 protein.
GN T24D18.27.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
RN
  (1)
  RC SEQUENCE FROM N.A.
  RC STRAIN=CV. COLUMBIA;
  RA Liu S.X., Yu G., Sakano H., Jhaveri A., Lee J.M., Lenz C., Pham P.,
  RA Toriumi M., Chin C., Chlou J., Choi E., Chung M., Gonzalez A.,
  RA Howing B., Koo T., Li J., Liu A., Vaysberg M., Altati H., Brooks S.,
  RA Buehler E., Chao Q., Conn L., Conway A., Hansen N., Johnson-Hopson C.,
  RA Khan S., Kim C., Lam B., Nguyen M., Palm C., Shinn P., Tambunga G.,
  RA Davis R.W., Ecker J.R., Federspiel N.A., Theologis A.;
  RT "The sequence of BAC T24D18 from Arabidopsis thaliana chromosome 1.";
  RL Submitted (SEP-1999) to the EMBL/Genbank/DBJ databases.
  RN
  (2)
  RC SEQUENCE FROM N.A.
  RC STRAIN=CV. COLUMBIA;
  RA Theologis A.;
  RL Submitted (DEC-1999) to the EMBL/Genbank/DBJ databases.
  DR EMBL; AC010924; AAF18513.1; -.
  DR HSSP; P02248; IUB1.
  DR InterPro; IPR000449; UBA_domain.
  DR InterPro; IPR000626; Ubiquitin.
  DR Pfam; PF00627; UBA; 1.
  DR Pfam; PF00240; ubiquitin; 1.
  DR SMART; SM00165; UBA; 1.
  DR SMART; SM00213; UBO; 1.
  DR PROSITE; PS50053; UBIQUITIN_2; 1.
  DR PROSITE; PS50053; UBIQUITIN_2; 1.
  SQ SEQUENCE 246 AA; 25966 MW; 0867D1E7D72B6FFE CRC64;

Query Match
Best Local Similarity 34.6%; Score 661.5; DB 10; Length 246;
Best Local Similarity 36.7%; Pred. No. 9,56-38;
Matches 143; Conservative 29; Mismatches 63; Indels 17; Gaps 4;

OY 1 MKLTVTKLGTGHEIRVOPNDITMAVKKNIETIOGDSYPMGQOLLIFNGKYLKDESTLE 60
DB 1 MKLTVTKLGTGHEIRVOPNDITMAVKKNIETIOGDSYPMGQOLLIFNGKYLKDESTLE 60
OY 61 ENKVNEDGFLVYMLSKGTSGTSSQSHSNTPATROAPLEAPQAPQPPVAPITTT 120
DB 61 ENKVNEDGFLVYMLSKGTSGTSSQSHSNTPATROAPLEAPQAPQPPVAPITTT 120
OY 121 PEGLPQAPNTDINAANLLSGRNVDTITNOLMEMGGSGMDKQORALRAAYNNPERAV 180
DB 109 VOEQPTAOSDTYGAQASTVSGSSISIEOMVQOIMEMGGSGMDKQORALRAAYNNPERAV 168
OY 181 EYLSGIPYTAET--AVPIGGAGNTTDRAPTEAGISGIPNTAPLDEPPQASNAGGAG 239
DB 169 DYLSGIPYTAET--AVPIGGAGNTTDRAPTEAGISGIPNTAPLDEPPQASNAGGAG 224
OY 240 GGPLDFLRNPPQ 251
DB 225 LGTLIELRGNQ 236

RESULT 11
ID Q8WUB0 PRELIMINARY; PRT; 409 AA.
AC Q8WUB0;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE RAD23 homolog B (S. cerevisiae).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
NCBI_TaxID=9606;
RN
  (1)

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RA Sulton G.G., Wolrtman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Chamne M., Pfeiffer B.D.,  
RA Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.L.G.,  
RA Abtill J.F., Agbayan A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,  
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
RA Beeson K.Y., Benos P., Berman B.P., Bhendari D., Bolshakov S.,  
RA Bockova D., Botchan M.R., Bouck J., Brockett P., Brotlier P.,  
RA Butris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
RA de Palos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
RA Dudon K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,  
RA Fioder C., Gabriellian A.E., Garg N.S., Galhart W.M., Glasser K.,  
RA Glaser A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,  
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeigwan C.,  
RA Jatalil M., Kalush F., Kapen G.H., Ke Z., Kennison J.A., Ketchum R.A.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
RA Lascko P., Lai Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Merkulov G., Mishina N.V., Mobery C., Morris J., Moshrefi A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclé J.M.,  
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Wang Z.-T., Wassarman D.A., Weinstock G.M., Weissbach J.,  
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
RA Ye J., Yah R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
RA Zhang X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,  
RT "The genome sequence of *Drosophila melanogaster*.",  
RL Science 287:2185-2195(2000).  
[2]  
RP SEQUENCE FROM N.A.  
RP Brodsky M.H., Rubin G.M., Teang G. :  
RT "Full length *Drosophila melanogaster* cDNA sequence.":  
RL Submitted (MAR-1999) to the EMBL/Genbank/DBJ databases.  
DR EMBL: AEO03844; AAF59352.1; -;  
DR EMBL: AF132147; AAD33594.1; -;  
DR HSSP: P54725; IDVO.  
DR FlyBase: FBgn0026777; Rad23.  
DR InterPro: IPR004806; Rad23.  
DR InterPro: IPR000649; UBA domain.  
DR InterPro: IPR000626; Ubiquitin.  
DR Pfam: PF00627; UBA\_2.  
DR Pfam: PF00240; ubiquitin\_1.  
DR PRINTS: PR01574; TUBBPROTEIN.  
DR SMART: SM00165; UBA\_2.  
DR SMART: SM00213; UBO\_1.  
DR TIGRFAMs: TIGR00601; rad23\_1.  
DR PROSITE: PSS0053; UBIOUITIN\_2; 1.  
DR PROSITE: 45780 NM; 1.  
SQ SEQUENCE 414 AA; 4C2EE494CA116F7AB CRC64;

	Query Match	25.5%;	Score 487.5;	DB 5;	Length 414;	
	Best Local Similarity	28.8%;	Pred. No. 1,6e-25;			
	Matches 128;	Conservative	78;	Mismatches 130;	Indels 109;	Gaps 11
QY	1	MLKLVKTLKGTHFEIRVQPNNDITMAVKNIEIQGRDYSYMGQOLLIFNGYLVKDESTLE	60			
		:   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :				
Db	1	MIITKINLQOQFTTEPAPEKTEVLTKKKIFEEGRPE-VYAEKOKILYGVILITDRRTYG	59			
QY	61	ENKVADEDFILVWMLSKGTSGSTGSSGSHN-----TPATRCAPPLPAAQAAPQ-----	111			
		:   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :				
Db	60	SYNDEKFFIVYMLLRDSSSSNRNOLSVYKESKTLTSTDGSKOSMPCDEAHNTNSPESTNT	119			
QY	112	-----VPAPITTSQPEGLPAQADPNTHDNAASNTLSCGNVDTIINQLMGEGGSDMDK	164			
		: : :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :				
Db	120	EDSVLSRETRPLSDELLIGELAAQ-SLGRASRNLLMGDEYINQYVLSWENG---YPRQ	175			
QY	165	VQRLRAAYNNDEPAAVEYLYSGIV-----TAEIAPVIGGAGANTTDRAPTGE	212			

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Db      176 VERMAASYNNEPERAVELLINGITIAEBCFTFYNNRNESTINSLIPSGQPMASISABERST 235
QY      213 AGLSGIPNTAFDLDFPGCASNAGGACAGGCPDLFTRRNPQOAVREMYHTNPQILOPMALVE 272
Db      236 -----SNSDPEEFTRSQPOFLQMRSLIYONPHLLHAVLQO 270
QY      273 LSKNPQOILRIEENHDEFILOLNEPF-----EGG----- 302
Db      271 IGTFTPALLOLITSENODAFILMLNQPLDRESESGATVPVSNARIPSTLDNDVLFSPDL 330
QY      303 -----EGDRLDPEEDMHPHLS---VYPEROEAIGRLESGFPRARY 342
Db      331 VATSAQRSACTSAAHSGSADND-EDLEGPGLGVSTIRLRQKDAIERKALGCFEDALY 389
QY      343 IEAFPLACDRNEELIANYILLERAGE 367
Db      390 LQATFACKEEQAANFLSSFFD 414

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ID	097135	PRELIMINARY:	PRT:	341 AA.
AC	097135:			
DT	01-MAY-1999 (TREMBLrel. 10, Created)			
DT	01-MAY-1999 (TREMBLrel. 10, Last sequence update)			
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)			
DE	Recp-binding protein A.			
GN	RCBA.			
OS	Dictyostelium discoideum (Slime mold).			
OC	Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.			
CC	NCBI_TaxID=44689;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-SLB153;			
RA	Li G., Alexander H., Alexander S.;			
RT	"rcba", the Dictyostelium discoideum homolog of yeast repair gene			
RT	Rad23."			
RL	Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.			
DR	HML: AF103870. YAD17913.1; "			
DR	HSP: P54725.1DY0.			
DR	InterPro: IPR004806; Rad23.			
DR	InterPro: IPR000449; DBA_domain.			
DR	InterPro: IPR000626; DBquitin.			
DR	Pfam: PF00627; UBA: 2.			
DR	Pfam: PF00240; ubiquitin; 1.			
DR	SMART: SM00165; UBA: 2.			
DR	SMART: SM00213; DBQ: 1.			
DR	TIGRFAMS: TIGR00601; rad23; 1.			
DR	PROSITE: PS50053; UBQUITIN_2: 1.			
SO	SEQUENCE 341 AA; 37528 MW; E376B909E6DE57E CRC64;			
Query Match	25.3%;	Score 484;	DB 5;	Length 341;
Best Local Similarity	30.6%;	Pred. No. 2.2e-25;		
Matches 119;	Conservative 65;	Mismatches 135;	Indels 70;	Gaps 9;
QY	1	MLKLVTKLGNHFEIRVQPNPTIMVKKNIIEIQKDSYPMQQLLIFNGKVLKDESTLE	60	
DB	1	MKVITKINKKEIYEVNGDLTALAKNLISL--KKNQTPSWQTLIYSGKLEKRTLE	57	
QY	61	ENKYNEDGFLVYMLSKGTSGSTSS-----QHSNTPATROAP	100	
DB	58	SYNLTDSGFIKMKIKKREAPATPATPTPLHLANTSTNNHHYCKTPNPHXLNTSTTT	117	
QY	101	PLEAPQAPORPVAFITTSQPEGLPAQAPNTHDNAASNLSCRNVDTIINQLEMGGGSW	160	
DB	118	PTSVPTPTNTPATPAPNPPTTSTSGTSTSGTSSPOQSDFAETGTELEAVIKNTDNG--F	174	
QY	161	DKDKVQRLRAAYNPKERAVEIYSG-IPVTAELIAPVIGGQCANITDAPATGEADLSGP	219	
DB	175	ARDVQRLRLRLTFNNAERLIVSGNIPAND-----PEDEEMEG--	216	
QY	220	NTAPIDLEPQASNAGGAGGAPLDELFRNNPQFQAVREKVNHTNPQILQPLVETLSKQNPQ	279	



Db	217	-----GGGSGGNPPEALRNHPHLLAEASKNSIIPGLQOLAQNPA	261
Qy	280	ILRLIENHDEFLQALNPEPBGCGDFLDQPEEDDMFHAISVPEQEOAIGRLSEMGFD	338
Db	262	LVRIOENPNFEIRLFO-----GGGN-----PGGNPGQFTLVQVQEESEAIQRIQALGMD	312
Qy	339	RARVIEAFIACDRNEELANYLEHAGEE	367
Db	313	KSTVIEAFACDRNEELASTLFTADE	341

